



```
LLANGESTGNSGSSGSGGATGSSQTSISGDVVEACCSVLVSMVCAADPVYKVTVAALKTLRLAMLVYTPC
|||||
LLANGESTGNSGSSGSGGATGSSQTSISGDVVEACCSVLVSMVCAADPVYKVTVAALKTLRLAMLVYTPC
580 590 600 610 620 630 640
HSLAERIKLQRLQPVVDITLVKCADANSRTSOLSTLLELCKGQAGELAVGREILKAGSIGIGVDVYLN
|||||
HSLAERIKLQRLQPVVDITLVKCADANSRTSOLSTLLELCKGQAGELAVGREILKAGSIGIGVDVYLN
590 600 610 620 630 640
HSLAERIKLQRLQPVVDITLVKCADANSRTSOLSTLLELCKGQAGELAVGREILKAGSIGIGVDVYLN
650 660 670 680 690 700 710 720
CILGNQTESNNWQELLCLIDLLELLEFAEFVPHIVSTDVSOAEFVEIRYKLLSLTLFALQSIDNSHSM
|||||
CILGNQTESNNWQELLCLIDLLELLEFAEFVPHIVSTDVSOAEFVEIRYKLLSLTLFALQSIDNSHSM
730 740 750 760 770 780 790
CILGNQTESNNWQELLCLIDLLELLEFAEFVPHIVSTDVSOAEFVEIRYKLLSLTLFALQSIDNSHSM
800 810 820 830 840 850 860
VGKLSRIYILSSARMVTVPHVFSKLEMLSVSVSTHFTMRRLMAYADEVEIAEAIQGVEDTLQROQH
|||||
VGKLSRIYILSSARMVTVPHVFSKLEMLSVSVSTHFTMRRLMAYADEVEIAEAIQGVEDTLQROQH
870 880 890 900 910 920 930
NSFCRHLPFTTIPQRTVPLECTVHLEKTKGKLCATKLSASSDIERLARISVGPSSSTTTTTTTEQPK
|||||
NSFCRHLPFTTIPQRTVPLECTVHLEKTKGKLCATKLSASSDIERLARISVGPSSSTTTTTTTEQPK
940 950 960 970 980 990 1000
PMVQTKGRPHSQCLNSPLSHSQMLPFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCPISASPTQKRF
|||||
PMVQTKGRPHSQCLNSPLSHSQMLPFPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCPISASPTQKRF
1010 1020 1030 1040 1050 1060 1070 1080
SLOFHRNCPENKSDKLSPTQSPRPSPSSNHRPKSRPTPGNTSKQDPSKNSMTLDLNSKSCDDSPGL
|||||
SLOFHRNCPENKSDKLSPTQSPRPSPSSNHRPKSRPTPGNTSKQDPSKNSMTLDLNSKSCDDSPGL
1090 1100 1110 1120 1130 1140 1150
SSNSNCCYTSDETVTFVEBKRLDVNTENSSIEDLLEASMPSSDTTVTFKSEAVLSPEKAENDTYKD
|||||
SSNSNCCYTSDETVTFVEBKRLDVNTENSSIEDLLEASMPSSDTTVTFKSEAVLSPEKAENDTYKD
1160 1170 1180 1190 1200 1210 1220
DVNHNOKCKEKKEAEAEALAIAMASQVALPIVPOLOQVENGEDIIIIQODTPETLPCHTKAKQPYREDT
|||||
DVNHNOKCKEKKEAEAEALAIAMASQVALPIVPOLOQVENGEDIIIIQODTPETLPCHTKAKQPYREDT
1230 1240 1250 1260 1270 1280 1290
EVLKQQIQLGAFSSCYQADVTGTLMAVKQVTVVRNTSSEQEVVEALREEMMHLNHPNIIIRMLGAT
|||||
EVLKQQIQLGAFSSCYQADVTGTLMAVKQVTVVRNTSSEQEVVEALREEMMHLNHPNIIIRMLGAT
1300 1310 1320 1330 1340 1350 1360
CEKSNYNLFIEWMAGSVAHLISKYGAFKESVWINYTEQLRGLSYLHNGIIRHDVKGANLLIDSTGQRLR
|||||
CEKSNYNLFIEWMAGSVAHLISKYGAFKESVWINYTEQLRGLSYLHNGIIRHDVKGANLLIDSTGQRLR
1370 1380 1390 1400 1410 1420 1430 1440
IADFGAARLAKSGTGAGFQQLIGTTAFMAPEVLRQOQIGRSQDVWSGCAIIEMACAPPNWAEKSHNH
|||||
IADFGAARLAKSGTGAGFQQLIGTTAFMAPEVLRQOQIGRSQDVWSGCAIIEMACAPPNWAEKSHNH
1450 1460 1470 1480 1490 X
LALIFKIASATTAPSIPLSHSPGLRDVALRCLELQPODRPPSRELLKHPVFTTW
```

```
|||||
LALIFKIASATTAPSIPLSHSPGLRDVALRCLELQPODRPPSRELLKHPVFTTWXLIQINIVETGCSRE
1450 1460 1470 1480 1490 X 1500 1510
KKLVGNHIDIYCHDATEQLXTRPVGNPYLSMXL
1520 1530 1540
```

2. US-09-697-898-3 (1-1495)  
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 16 Optimized Score = 53 Significance = -0.40  
Residue Identity = 23% Matches = 81 Mismatches = 130  
Gaps = 139 Conservative Substitutions = 0  
Translation Frame = 4

X 10 20  
PSPEAGGGGALKASSARAAAA

LLQSGKXALSAAVSTVMPASLCKHGLFPQGYMVRSHLVKGLFGVXVCHSEKA---LGKLFSLLELLI  
1260 1270 1280 1290 1300 X 1310 1320

30 40 50 60  
GLLRAGSGGRERADWRRLQRLK---VRSVELDQI-----PEQPLFLA-ASPP---AS-----  
SLCDLWGS-CQEKDCVGLWKLVPKPLPGPLLETQLLSDSFQIHLXGLVLPQALAYFSPTTPASPLAYR  
1330 1340 1350 1360 1370 1380 1390

70 80 90 100 110 120  
--STSP-SPEPADAAGSGTGQFVAVPPPHGAASRRG-AHLTESVAAP-----DSGASSPA--AAEPG  
LFSVPKSPVPLDDHPSCATLXEFLYSPSH---DRGQLOETARRRASPAPRRLRDSRRCPAPPTRXG  
1400 1410 1420 1430 1440 1450 1460

130 140 150 160 170 180  
EKRAAAEPSPAAAAGREMENKTLKGLHKMDRPFBERMIREKLKAT---CMPAWKEWLERNNR-----  
GRRA-GWELRGAAAPPOAGSRSHSL-----RP-----RAPATGKSRPA-----VRQGRAAAQA  
1470 1480 1490 1500 1510

190 200 210 220 230 240 250 260  
-GPVVVVKPIPVKGDGSEMHLAAESPGEVQASASPAGSKRRSPSGNSPGRVKSSEPGVRRKRVSPVPF  
AGP-----APHSALCAAAAASPPARGPRCPDP-----AAVPR  
1520 1530 1540

270 280 290 300 310 320 330  
QSGRIITPPRAPSPDGFSPSYSPETNRRVKNVNRARLYLLOQIGNSLIGDSDPNKIRVFIGPQNSCAH  
Q-----PRARCSPXG-----LIR-----RLPQG  
1550 1560 X

340 350  
GTFCIHLLFVMLRVFOLE

3. US-09-697-898-3 (1-1495)  
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 14 Optimized Score = 56 Significance = -0.40  
Residue Identity = 26% Matches = 72 Mismatches = 133  
Gaps = 68 Conservative Substitutions = 0  
Translation Frame = 6

X 10 20  
PSPEAGGGG--GALKASSARAA

LTRRFVSSGLYGEKPSGEGALRGGVILPLXKGTGETFLTLTPGDSDFTVRPGELPGEGLRPLEAGEALA  
1280 1290 1300 1310 1320 X 1330 1340

30 40 50 60 70  
-----AAGLLREAGS---GGRERADWRRLQRLKRVSVELDQLEPQPLFLAASPPASTSPS-----

WTPGDSAAKFIPIPSPLTIGITGTTGPRFLLSNHS--CFQAGIQVAFSFLIIRSSGSSILCNPLRVS  
 1350 1360 1370 1380 1390 1400 1410  
 ----PEPADAAGSGTGFPQVAVPPHGAASRRGAHLTESVAAPDS--CASSPAAAEPCERKAPAAERSP-AA  
 80 90 100 110 120 130  
 LPSISRPAGAA--AGDGAAGARFSPGSAAGLEAPL--SGAATSVKAPRELAAAPWGGGTATGKQVPLPA  
 1420 1430 1440 1450 1460 1470 1480  
 140 150 160 170 180 190 200 210  
 APAGEMENKETLGLHOMDORPEERIMIREKLKATCMPAKHEMLERENRRGPPVVVKPIPVKGGSGSMNHLA  
 ASAG-----SGDGEVEAGGEAARKSCGSGSSSTL-RTLR-----SCRRRQS  
 1490 1500 1510 1520  
 220 230 240 250 260 270  
 ABSPEGEVQASAAASPASKR-----RSPSPGNSPSTGRTVKSESPPGVRKRVSPVFPQSGRITPPRRAPSPDGF  
 ARSRPPLPASRSPPAAARALALRAP-PPPPASG  
 1530 1540 1550 1560 X  
 280 290  
 SPYSPEETNRRVN

4. US-09-697-898-3 (1-1495)  
 US-09-359-756-1 Sequence 1, Application US/09359756  
 Initial Score = 9 Optimized Score = 246 Significance = -0.41  
 Residue Identity = 21% Matches = 374 Mismatches = 846  
 Gaps = 559 Conservative Substitutions = 0  
 Translation Frame = 3

X  
 PSPE-----AGGGGALKAGSARAAAAGLLREAGSGRRERADWRRRL-----  
 EPXGRRRRSPQEQPARCGRGTAGGGGGRPRAGGLAATAAQAEGCAGPAAAXAALPCELTAGLADFPV  
 10 20 30 40 50 60 70  
 50 60 70 80 90 100 110  
 --RKVSVELDQLEQPLFLAASPASSTSPSPADAGSGTGFPVAVPPHGAASRRGAHLTESVAAPD  
 AGARGSGEWDRLP--ACGGAAP--RSQPARPPYRVGGGAG--QRRLESRSGRA--RGEGARRRAVSC  
 80 90 100 110 120 130  
 120 130 140 150 160 170 180  
 SGASSPAAAEPCERKAPAAEPSPAAAPAG-----REMNKETLGLHOMDORPEERIMIREKLKATCMPAKHE  
 SG--PRRSDGEXR-----NSQVADQKSGSRGTNDQGETGNL--YASLEARM-VGKEXKARACGKTN  
 140 150 160 170 180 190  
 WLRR-----NRRGP-VVVKPIPVKGGSGSMNHLAESPGEVQASAAASPASKRRSPSPGNSPSGR  
 190 200 210 220 230 240  
 PSXRRWIXNESLSSXVSRGPGKGTSPQRTQSPFSWQLPIRSHSEIRIS-----RSKEKKGFPAGFSEWQN  
 200 210 220 230 240 250 260  
 TVKSESFGVR-----RKRVSPPVFPQS-----GRITPPRA-PSPDGFSYSPSEETNRR-----VNVKMPA-R  
 250 260 270 280 290 300 310 320  
 HTTPKSPFTWLLTIXPGNKPCQSDAGQTLTAADRAXLFPD-----WRRQXQIFGVYWASE  
 270 280 290 300 310 320  
 300 310 320 330 340 350 360  
 LYLLOIGFNSFLIGDPSPNKTRVFIGPQNCSCAGTFCIHLLFWMLRVFQLEPSDPMWLKTLK-----  
 LQICTWNILYSSAI-CDAPGVSTRTP-RPNVMEKNFKEF-XGAEFV-----PEIS-----QXAXLKQSSIS  
 330 340 350 360 370 380  
 --NFEVESLQKYHSRRSRRIKAPSRTI-----QKFSVRMSNSHTLSSSSTSSSENISKDEEQMCPICL  
 370 380 390 400 410 420  
 XHPEVCVTHVK-----FSYIVIXFYIXRQKHGXGRTDVSLLVGHAXXKRSYSVARRLQEQAAP-----

390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590  
 LGMDBESTVCEDEGCR--NKLHHCMS--IWAE-----ECRRNREPLICPCRSKWSHDFYSH  
 ----PLHV-NLGRVVKXKRTFNMSPLIXVEISXFLQPRVVKSCGFPFFPQSCCTAANRTAAAFGWITK  
 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590  
 ELSSPVDSPESSL-RAAQOQTVQOQPLA-----GSR-RQNESFNMLTHYGTQ-----QIPAYKDLAEPW  
 E-SREOFXPYSLWNSNAPSCLOFAXMDSGVWNGTRWLLIFXKLECEDRDGPQASFPXQWGPVAVKQGEHW  
 520 530 540 550 560 570 580 590  
 IQVFGHELVCLFSRWNVNREMLRR-----LSHDV-----SGALLANGESTGSGSSGSSPSG-G  
 550 560 570 580 590  
 KFWGQWQKQPEWGSOWVFPDQVLRRCGGMLQORSYNGLCXPCQLQVRCFCFNIES--HAGIYSLPQFGKN  
 590 600 610 620 630 640 650  
 600 610 620 630 640 650  
 ATSGSSQTSISGDVVEAC--CSVLSWV-----CADPVYKYVAALKTLRAMLVYTPC-----HSLAE  
 OTSETSPASCRHHPSPQWRCQCPHKSAAVHINTVGTQVORPSRRVSGSHQRTKSWIHHYWCXLCCLKLYSNKPN  
 660 670 680 690 700 710 720  
 RIK-LQRLQPS-----VV-----DTILVKCADANSRTSLS-STILELCKGQAGELAVGREILKAGSIGGG  
 660 670 680 690 700 710  
 XIKQLARTSPPLSYRXTVVGISXIL-----SSYCYXCF--SKACXNOYKAAVPLNLCA-----VH  
 730 740 750 760 770 780  
 VDVYVNLGILQNTESNNWQELLGLCLIDLELLEFAEFY--PHIVSTDVSOAEPVEIRYKLLSLTLTFALQ  
 XXPELN--GWQT-----FOKDL-----LEFCNGYVSTPCVFTVRNAE-----CFQCFSHSHQDA--  
 790 800 810 820 830  
 790 800 810 820 830 840  
 SIDNSHSMVGLKERRIYLSGARVMT-----VPHVFSKLEMLSVSS--VSTHTTRMRRLMAVADE---  
 SPFDGLCRXGNCGRSHPVGRRRHFTTTTQQLQASVPNNYLETTNSSPXVHSPPREWKRMKCMYKIECOF  
 840 850 860 870 880 890 900  
 850 860 870 880  
 -VEIAEAIQ-----LGVEDT-----LQOQHNSFCRHL-----FP--TTIWKPORTVP---L  
 890 900 910 920  
 ECTVHLEKTKGK---LCAT-----KLS-----ASSEDISERLA-----RISVGP-  
 980 990 1000 1010 1020 1030 1040 1050  
 HCNRLAXATSGIHSLQNTFCISSNTAQVFTTIPQKLSXKQRLXRTTPPSLYSVKTLAQHTQAKALSTYPR  
 980 990 1000 1010 1020 1030 1040 1050  
 ----SSSTTTTTTTEOKPM-----VOIKGRPHSCLNSSLPLS-----HHSQLMFPALS-----  
 XYKXTGRSLKXKHDTXGEQFQWXXQLWLESCQXXLLLYQXRDVSHPSRGEMQIRCOYRAQLQXGSPXSIIY  
 1060 1070 1080 1090 1100 1110 1120  
 ----TPSSSTSPVPAG-----TATDVSK-HRLOG-----FIPC--RIPSASP-----QTORK  
 AFKYNNSPVRSCTPVSKXKXXYLQRCESXSKVQREDGSGVRRRSFNCNCHNVSVSGSPPHSSSAAGXK  
 1130 1140 1150 1160 1170 1180 1190  
 1010 1020 1030 1040 1050 1060  
 FSLQFHRNCENKSDKLSVPFT-----OSRPLPSNIHRPKSPRPTPGNTSKQGDPSKNSMTLDLN  
 WRRVHHYSTGTTRDSTRYQSKTTVXRHHXMAERSTDRPKSIFELLSSGR--CGNMVNG-----CXTGDL-  
 1200 1210 1220 1230 1240 1250

1070 1080 1090 1100 1110 1120  
SSSKCDDSGFGLSSNSCCYTSDETVTPVE-EKCRLDV-----NTEINS-----SIEDLLE  
-CQKHIFXARRSRSTRKRDNDE-----PSESSKHDXDVSHVKEQLOSLHXMGRG-GGSFAXKWSLQR  
1260 1270 1280 1290 1300 1310 1320  
1130 1140 1150 1160 1170 1180 1190  
ASMPSSDTTTFKSEVAVLSPERAENDDTYKDDVNNOKCKEVEA--EEEBALAJAMASASQVALPIVPO  
ISSYXLHXITVTPFTV-----SPXK-----PNSQRCQCFANXQHWSETKNCRCFWSCSQVGIKRWNC  
1330 1340 1350 1360 1370 1380  
1200 1210 1220 1230 1240  
LOVENGEDIIIQQDTPETLPHTKAKQPRE---DTEMLKGOQIGL-----GAFSSC-----Y  
RRV-----SCTIIGDCNIYCTGKTSKRWKELXCMECMLCYRNGLCCTMBECRTLOSFCFDIXDCXNY  
1390 1400 1410 1420 1430 1440 1450  
1250 1260 1270 1280 1290 1300 1310  
QAQDVGTGLMAVQVTVYRNTSEOEVEALREERIMSHLNHNIIRMLGATCEKSNYNLFIEWMAGGS  
CSIDPFT---FVSWFT---RCGSS-----LFRSTSGQTSIKR---AT-EAS-----S  
1460 1470 1480  
1320 1330 1340 1350 1360 1370 1380  
VAHLLSKYAFKESVINYTEQLRLGLSYLHENQIHRDVKGANLIDSTGQRLRADFGAARLASKGTGA  
-----LSY-----MVANYTDQLRR-----NRMNKRKK-----TCGEPHYXLRPXCHXTAMNEAS-----  
1490 1500 1510 1520 1530  
1390 1400 1410 1420 1430 1440 1450  
GEFGQLGTIAFNAPVLGQQVGRSCDVNSGCAIEMACAKPWPNAEKSHNLALFKIASATARSIP  
GE-----PLPKYVIDKSXSV-----PKLSMOK-----PKLVOK-----X  
1540 1550  
1460 1470 1480 1490  
SHLSPGLRDVALRCLELQPDPRPSRELLKHPVPTTW

5. US-09-697-898-3 (1-1495)  
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 9 Optimized Score = 50 Significance = -0.41  
Residue Identity = 22% Matches = 76 Mismatches = 153  
Caps = 116 Conservative Substitutions = 0  
Translation Frame = 5

TAAVLRPNKHPVFIWAVSSNQERVRPVLQXVOSGPHFVNTAVCFRLAIWKEAIWXRG-----SSGWCDSA  
1240 1250 1260 1270 1280 1290 1300  
X  
PSPEAGGGGALKASARAAAA  
30 40 50 60 70  
GLLRAG---SGGRER-----ADRRRLQKRVRSVELDQLPEQLFLAAGPPAS-----STS-----  
TLKXHWGNSFPSPYWRPFHFCATKXGVARRTASAFGSWSRTCLDL--SWRLSCXVIHFRSISFNWDFYH  
1310 1320 1330 1340 1350 1360 1370  
80 90 100 110 120  
--PSP---EPADAGSGTG---FQP-----VAVPPHGAASRGAAHLTESVAAPDSGASSPAAAPPG  
HRPSPISPPFVLPFGMHTGCLQLPDHSFLLWTHLVOP---FESFFILHLLTGGGRCRRRLGGGRPLLP  
1380 1390 1400 1410 1420 1430 1440  
130 140 150 160 170 180  
EKR---APAA-----EPSPAAAPAGRENMENKTLKGLHKMDRDRPEERMIREKLCATCMPAKHWELERRNR  
1450 1460 1470 1480 1490  
LGRCTRGAAVRRRRLKGVGAAPAG-----GSGVRRHRLEAQPTP--RCVRLGLRRGS

190 200 210 220 230 240 250 260  
RGVVVKPIPVKGDGSEMNHLAABSPGEVQASAAASPASKGRRSPSPGNSPGRVTKSESGVGRKRVSPVPF  
RG-----GRRXGKGEERLL-----ROLVOLHTPHFA-----QLPPPPVRP-----LAAFAAR-----LQO  
1500 1510 1520 1530 1540  
270 280 290 300 310 320 330  
QSGRITPPRAPSPDGFSPSPYSPPEETNRVNVKVMRARIYLLOQIGPNSFLIGGSDPNKYRVFIGPQNCSEAH  
QS-RGSR-ARAARLEGSS-----AAACLEA  
1550 1560 X  
340  
GTFCIHLLFVMLR

6. US-09-697-898-3 (1-1495)  
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 9 Optimized Score = 251 Significance = -0.41  
Residue Identity = 20% Matches = 359 Mismatches = 911  
Gaps = 456 Conservative Substitutions = 0  
Translation Frame = 2

X 10 20 30 40 50  
PSPEAGGGGALKASARAAAAAGL-----LREAG--SG-----GREER-----DWRRLQKRVRSVELDQLPEQ  
RALRQAAAEPSRAAARLPRDCCGRRAAGAAAGRTGGGGSCAKCGVWWTSCLSRSSSLPHRRPP  
X 10 20 30 40 50 60  
60 70 80 90 100 110 120  
PLFLAASP-----PASSTSPSEPADAAGSGTGFPVAVPPPHGAASRRGAHLTESVAAPDSGASSPAA  
RLPRRSPTRGVGPASSLWRCRP-----TEPPAGAAPTLPSEWRRTAAP-----RVQORP  
70 80 90 100 110 120  
130 140 150 160 170 180 190  
EPG-EKRAPAAEPSPAAAPAGRENMENKTLKGLHKMDRDRPEERMIREKLCATCMP-----AKHWELERRNR  
SPGRSRPPPSRLQRPVVRWRIKLSKCTRWMIVORNEXSGRXNQPVQCPGSGTNGKGBIGELGMWX  
130 140 150 160 170 180 190

190 200 210 220 230 240 250  
GPPVVVKPIPVKGDGSEMNHLAABSPGEVQASAAASPASKGRRSP---SPGNSPGRVTKSESP-GVARKRV  
NQSQLKEMDLK-XITXQLSLQERSQVRLHQLPKA-DAVLLATPHQVAXNQNLQEXGEKEFFQCLFRVAE  
200 210 220 230 240 250 260

SPVP-----FQSGRI-----TPERRAPSPDGFSPSPYSPPEETNRVNVKVMRARIYLLOQIGPNSF  
SHHPPEPLHQAASHHIALRKQTAVLTXXCGPDCTYCSRXGLTLXLEETAQTINTGCLLGLRTAAVHMS-  
270 280 290 300 310 320 330  
310 320 330 340 350 360 370 380 390  
LIGGSDPNKYRVFIGPQNCSE-----CAHGTFC-----IHLFVMLR---VFQLEPSDPMWRKTLKNF--  
-----VFICYLXCSGCFNXLQTCYGEKLRILRLRVCSRNITVGVAAQSKLHLVTPSRSLFHA  
340 350 360 370 380 390  
-----EVESLFOKVHNR--RSSRIKAPSRNTICKFYVRNSNHTLSSSTSTSSSENSIODEEQMC  
400 410 420 430 440 450 460  
CQILIHCHHLVLLHLVQKTAHMKNRNRCVLFACWACLWKV--LOCVTAAGTCTTTACQPGQKSVBE---  
430 440 450 460 470 480 490  
PICLLGMLDEESITVCEDCGRNKLHHHCHMSIWAEECRNRNREPLICPLCKRSKWRSHDFYSHELSSVSPSSSL  
-IENL-----XYVPFVDLSGDLMISTATSC-----QVLWIPFLPSELHSSKPYIS--SSLWLDHEGIX  
470 480 490 500 510  
500 510 520 530 540 550

RAAQOQTVOOQPLAGS-----RRNOESFNLTHTYQTOIPPAYKDLAPW-IQVFMGLVGCFLFS  
||  
RA--ILTLIMELSKSLTLTXILSHGPRCLEW--SLAAY-----FLETGMKRWSPGVFMMSVG-----P  
520 530 540 550 560 570  
560 570 580 590 600 610 620  
NNWVEMALRRLSHDVSGALLANGESTCNGSGSGSPSGCATSGSQTSGSDVVEAC-CSV--LSMVCA  
CWQMGRALEITLGAAVEAA--RVGE-----PPVGLPRPVSPQENMWRHAAAFQOWSVLTLSTKC-  
580 590 600 610 620 630  
630 640 650 660 670 680 690  
DPVKYKYVAALKTLERAMLVYTPC--HSLA-----ERIKQLQLLOP-----VVDTI--LVKC-----A  
-----TLXLXHXHPCWILLATVTKESNFRDSSQLXTPSKSNVOMPAAQVSCPQHCWNCNA  
640 650 660 670 680 690  
DANSTSQ-----SISTLELCKGQAGELAVGREILKAGSIGI--GGVDYVLNCLIGNQT  
700 710 720 730 740 750  
KAKQESWOLAEKYYKLDPLVLVWLIMSXIVLETKNO-----TIQKQFLAFVLXIDCCWNFLLNFIILSV  
760 770 780 790 800 810 820  
ESNNWQELL--GRCLIDRLILLEPP-----AEFYPHIVSTDVSO-----ABPV-----  
730 740 750 760  
LMFHKLILKSGIRSCCPXLLCPLIPTQMLANF--PEGSTXVLQEWLLOYCMCFQNCXKCKXVPFPPL  
760 770 780 790 800 810 820  
TSPGCVAVXWLMOMRWKLPKPPSSWAXKTLNDNNNTAFAGICS--QQLSGNHRQOFLPSAQSIKXLEKDYV  
830 840 850 860 870 880 890  
830 840 850 860 870 880 890  
--SSYSTHTRMRRLMAYADVEIAEAIQLGVEDTLQROHN--SFCRHLFT-----TIWKP  
LQNXVPVORTFLRDWPGFOX-----LLVQOQOQOQSQNSQMFQKQADPTSVXTPLLYLIIPNCKF  
900 910 920 930 940 950 960  
QRTVLECTVHLEKTKGICATKLSASSED--ISERLARISVGPSS--STTTTTTITEQ-----  
880 890 900 910 920 930  
QPCQPLLLPHL--YQLAQOWSLSIDFRDSPAPBYLLHLKHGSFLYNSTETVLKTKTOINFPQSLLSQD  
970 980 990 1000 1010 1020 1030  
940 950 960 970 980 990 1000  
PKPMQTKGRPHSQCLNSPLSHHQLMFPALSTSSSTPSVPAGTATDVSKHRLQGFICRIPRISAPQTOR  
PCPPVYTQGS--LPLQVQVNRNIEPOKIAHLIXTVPNV--MTALAXAAIIVVIAVIP-VTRQCSPOKXR  
1040 1050 1060 1070 1080 1090 1100  
1010 1020 1030 1040 1050 1060 1070  
---KESLQPHRNCPENKSDKLSPVFTQ---SRPLPSSNIHRKPSRPTPGNTSKQGDPSKNMSTDLNSSS  
NADXMSIQSTSVLRTFLKHLCLQVIOQKLSLQKLSLKLKXWMIPT-----KMXIIKSAKRKKWLKK  
1110 1120 1130 1140 1150 1160  
1080 1090 1100 1110 1120 1130 1140  
KCDSDSGLSSNSNCCYTSDETVFPVBEKCLDVNTLNS--IEDLEASMPSSDITVTTFKSEVAVLS  
K-----KLXQLPWC--ORLXPSPXFLSCRL--KNEKISLFRNIHQRIYQDIP-----KQNNR  
1170 1180 1190 1200 1210 1220 1230  
1150 1160 1170 1180 1190 1200 1210  
PEKAENDTYKDDVN-----HNQKCKERKEAEFEALAIAMASQVALPIVPOLQVE--NGEDITIIQ  
1200 1210 1220 1230 1240 1250 1260  
IEKTLN---GKXNFXALEHLLVIRLQWBLELXWLLNRLXMSETHLLSKKXXKXKEXKXAIIXIO  
1220 1230 1240 1250 1260 1270 1280  
1210 1220 1230 1240 1250 1260 1270  
QDTPETLPGHTKA-----KQPYR-----EDTELWKQOQIGLAFS-----SCYQAQDVGTGT  
1240 1250 1260 1270 1280 1290 1300

> O <  
O||O IntelliGenetics  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 6168950\_x\_697898.res made by spaula on Thu 20 Feb 103 16:41:15-PST.

Query sequence being compared: US-09-359-756-1 (1-4693)

Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-359-756-1 (1-4693) with:  
File : US09697898mod.psp

```

100-
-
N U 50-
M -
B E 10-
E E 5-
R -
-
O F 10-
-
S -
E E 5-
Q U -
-
E -
N -
G -
E -
S 0-

```

SCORE 0 167 333 500 666 833 999 1166 1332 1499  
STEEV

## PARAMETERS

Similarity matrix Unitary K-tuple 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 500  
Gap size penalty 0.05  
Cutoff score 0  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean Median Standard Deviation  
1499 0 0.00  
Times: CPU  
00:00:00.00 Total Elapsed  
00:00:00.00

Number of residues: 1495  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Sig. Frame  
Init. Opt.  
-----  
1. US-09-697-898-3 Sequence 3, Application US 1495 1499 0.00 1

1. US-09-359-756-1 (1-4693)

US-09-697-898-3 Sequence 3, Application US/09697898

Initial Score = 1499 Optimized Score = 1499 Significance = 0.00  
Residue Identity = 100% Matches = 1495 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0  
Translation Frame = 1

```

X 10 20 30 40 50 60 70
PSPEAGGGGALKASSARAAAAGLLREAGSGGRERADWRRQLKRVRSVELDQLPEQLFLAASPPASSTSP
PSPEAGGGGALKASSARAAAAGLLREAGSGGRERADWRRQLKRVRSVELDQLPEQLFLAASPPASSTSP
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
SPEPADAGSGTGFPVAVPPPHGAASRRGAHLTBSVAAPDSGASPPAAAFGEKRAFAAEPSPAAAPAGRE
SPEPADAGSGTGFPVAVPPPHGAASRRGAHLTBSVAAPDSGASPPAAAFGEKRAFAAEPSPAAAPAGRE
80 90 100 110 120 130 140
150 160 170 180 190 200 210
MENKETLKLHKMDRPERMIREKLKATCMPAWKHEMLERNRNGPVVVKPIPVKDGSEKNNHLAASPGE
MENKETLKLHKMDRPERMIREKLKATCMPAWKHEMLERNRNGPVVVKPIPVKDGSEKNNHLAASPGE
150 160 170 180 190 200 210
220 230 240 250 260 270 280
VQASAASPASKGRSSPSCNPGRTVAKSESGVRRKRVSPVPPFOSGRITPPRAPSPDGFSPYSPEETNRR
VQASAASPASKGRSSPSCNPGRTVAKSESGVRRKRVSPVPPFOSGRITPPRAPSPDGFSPYSPEETNRR
220 230 240 250 260 270 280
290 300 310 320 330 340 350 360
VNKVMARLYLLOQIGPNSFLIGGSDPNKYRVFIQPNCSCAHGTFCIHLFLVMLRVFQLEPSPDMLWRKT
VNKVMARLYLLOQIGPNSFLIGGSDPNKYRVFIQPNCSCAHGTFCIHLFLVMLRVFQLEPSPDMLWRKT
290 300 310 320 330 340 350 360
370 380 390 400 410 420 430
LKNFEVESLFQKYSRRSRRIKAPSNTIQTQKFSRMSNSHTLSSSSTSSSENSIKDEEQMCPICLLGML
LKNFEVESLFQKYSRRSRRIKAPSNTIQTQKFSRMSNSHTLSSSSTSSSENSIKDEEQMCPICLLGML
370 380 390 400 410 420 430
440 450 460 470 480 490 500
DEESLTVCEGDCGNKLHHCHMSIWAEECCRNREPLICPLCRSKWRSHDFYSHELSPVSPSLRAAQOQTV
DEESLTVCEGDCGNKLHHCHMSIWAEECCRNREPLICPLCRSKWRSHDFYSHELSPVSPSLRAAQOQTV
440 450 460 470 480 490 500
510 520 530 540 550 560 570
QQOPLAGSRNRQSNFNLTHTYGTQQIPPAYKDLAEPWIVFGMELVGCFLFSRNNVREVALRRLSHDVSGAL
QQOPLAGSRNRQSNFNLTHTYGTQQIPPAYKDLAEPWIVFGMELVGCFLFSRNNVREVALRRLSHDVSGAL
510 520 530 540 550 560 570
580 590 600 610 620 630 640
LLANGESTGNSGGSSGSGGATSGSSOTSISGDVVEACCSVLMSVWCADPVYKTVVAALKTLRAMLVYTPC
LLANGESTGNSGGSSGSGGATSGSSOTSISGDVVEACCSVLMSVWCADPVYKTVVAALKTLRAMLVYTPC
580 590 600 610 620 630 640
650 660 670 680 690 700 710 720
HSLAERIKLQRLIQPVVDITLVKCADANSTLSLSISTLLEICKGAGELAVGREILKAGSIGGVVDVYLN
HSLAERIKLQRLIQPVVDITLVKCADANSTLSLSISTLLEICKGAGELAVGREILKAGSIGGVVDVYLN

```

650	660	670	680	690	700	710	720
CILNQTESNNQELLGRCLCUIDRLLEFFPAEFYPHIVSTDVSOAEVEIYRKKLJSLUFLFALQSDINDSHSM	730	740	750	760	770	780	790
CILNQTESNNQELLGRCLCUIDRLLEFFPAEFYPHIVSTDVSOAEVEIYRKKLJSLUFLFALQSDINDSHSM	730	740	750	760	770	780	790
800	810	820	830	840	850	860	
VGKLSRRILYLSARWTVTPHVFSKLEMLSVSSVSTFTMRRLMAYADEIAEAIOLGVEDTLQROQH	800	810	820	830	840	850	860
VGKLSRRILYLSARWTVTPHVFSKLEMLSVSSVSTFTMRRLMAYADEIAEAIOLGVEDTLQROQH	800	810	820	830	840	850	860
870	880	890	900	910	920	930	
NSFRCHLPFTTIIMKQRTVPLECTVHLEKTKGKICATKLSASSEDISERLARISVGPSSSTTTTTTTEQPK	870	880	890	900	910	920	930
NSFRCHLPFTTIIMKQRTVPLECTVHLEKTKGKICATKLSASSEDISERLARISVGPSSSTTTTTTTEQPK	870	880	890	900	910	920	930
940	950	960	970	980	990	1000	
PMVQTKGRPHSQCLNSSPLSHHSQMLFPALSTPSSSTPSVPAGTATDVSKHRLGOGFIPCRIPASPOTQKRF	940	950	960	970	980	990	1000
PMVQTKGRPHSQCLNSSPLSHHSQMLFPALSTPSSSTPSVPAGTATDVSKHRLGOGFIPCRIPASPOTQKRF	940	950	960	970	980	990	1000
1010	1020	1030	1040	1050	1060	1070	1080
SLOFHRNCPENKDSKLPVPTQSEPLSSNIHRPKSPRPFGNNTSKGDPSPKNSMTLDLNSSSKCDSDSGL	1010	1020	1030	1040	1050	1060	1070
SLOFHRNCPENKDSKLPVPTQSEPLSSNIHRPKSPRPFGNNTSKGDPSPKNSMTLDLNSSSKCDSDSGL	1010	1020	1030	1040	1050	1060	1070
1090	1100	1110	1120	1130	1140	1150	
SSNSNCCVTSDETVTFVEEKCRLDVNTLNSSIEDLEASMPSSDITVTFKSEAVLSPKEAENDDTYKD	1090	1100	1110	1120	1130	1140	1150
SSNSNCCVTSDETVTFVEEKCRLDVNTLNSSIEDLEASMPSSDITVTFKSEAVLSPKEAENDDTYKD	1090	1100	1110	1120	1130	1140	1150
1160	1170	1180	1190	1200	1210	1220	
DYNNHCKCKEYEBEEBALAIAMWASQVALPIVPOLOVENGEDIIIIQODPETLPGHTKAKQFREDT	1160	1170	1180	1190	1200	1210	1220
DYNNHCKCKEYEBEEBALAIAMWASQVALPIVPOLOVENGEDIIIIQODPETLPGHTKAKQFREDT	1160	1170	1180	1190	1200	1210	1220
1230	1240	1250	1260	1270	1280	1290	
EWLKGQOIGLGFSSCYQADQVGTGLMAVKOVTVYRNTSDQEEVVEALREIIRMMSHLHNPNIIRMLGAT	1230	1240	1250	1260	1270	1280	1290
EWLKGQOIGLGFSSCYQADQVGTGLMAVKOVTVYRNTSDQEEVVEALREIIRMMSHLHNPNIIRMLGAT	1230	1240	1250	1260	1270	1280	1290
1300	1310	1320	1330	1340	1350	1360	
CEKSNYNLFIEWAGGSVAHLLSKYGAPKESVIVNYTEQLLRLGLSYLHENQIIHRDVKAGNALLIDSTQORLR	1300	1310	1320	1330	1340	1350	1360
CEKSNYNLFIEWAGGSVAHLLSKYGAPKESVIVNYTEQLLRLGLSYLHENQIIHRDVKAGNALLIDSTQORLR	1300	1310	1320	1330	1340	1350	1360
1370	1380	1390	1400	1410	1420	1430	1440
IADFGAARLASKGTGAGBFQGLLGTIAFMAPVLRGQCYGRSCDQSVSGCAIEMACAKPPWNAEKSHNH	1370	1380	1390	1400	1410	1420	1430
IADFGAARLASKGTGAGBFQGLLGTIAFMAPVLRGQCYGRSCDQSVSGCAIEMACAKPPWNAEKSHNH	1370	1380	1390	1400	1410	1420	1430
1450	1460	1470	1480	1490	X	1500	
LALIFKIASATTAPSPHSLSPGLRDVAURCLQELQDPDPPSRELLKHPVFTTXXPIQINYVETGCGSTR	1450	1460	1470	1480	1490	X	1500
LALIFKIASATTAPSPHSLSPGLRDVAURCLQELQDPDPPSRELLKHPVFTTXXPIQINYVETGCGSTR	1450	1460	1470	1480	1490	X	1500
1520	1530	1540					
KCLVGNHDIYDGHDATEOLXTRVGNPYSMXL	1520	1530	1540				

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 6168950 x 697898.res made by spaula on Thu 20 Feb 103 16:41:37-PST.

```

Query sequence being compared:US-09-359-756-1 (1-4693)
Number of sequences searched: 1
Number of scores above cutoff: 1

```

Results of the initial comparison of US-09-359-756-1 (1-4693) with:  
File : US09697898mod pep

Letter	Percentage
N	100%
D	50%
M	10%
E	10%
R	10%
Q	10%
P	10%
S	10%
E	10%
O	10%
D	10%
E	10%
N	10%
C	10%
E	10%
S	10%







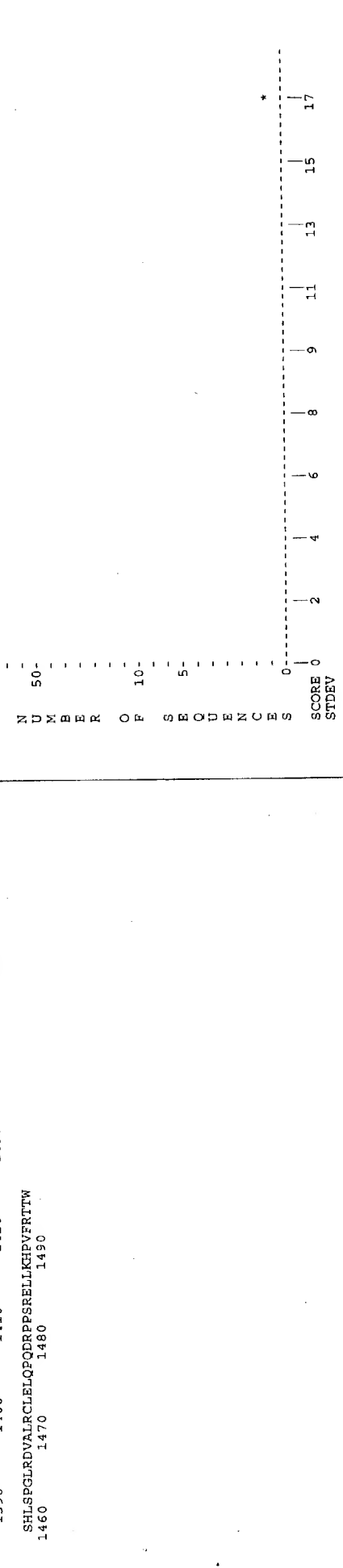
The list of best scores is:

Sequence Name	Description	Length	Score	Significance	Init. Opt.
1. US-09-697-898-3	Sequence 3, Application US	1495	10	263	0.00
1. US-09-359-756-1 (1-4693)					
US-09-697-898-3	Sequence 3, Application US/09697898				
Initial Score = 10	Optimized Score = 263			Significance = 0.00	
Residue Identity = 21%	Matches = 374			Mismatches = 846	
Gaps = 559	Conservative Substitutions = 0				
Translation Frame= 3					
10	20	30	40	50	60
EPXRRRRSPQGEQARGCRTAAGGQGRPRAGGLAAQAAGSFCAGPAAKAAALPCRLTAGLDFPV					70
PSFE-----AGGGGALKASSARAAAAGLLRAGSGGRERADWRRL-----					80
X	10	20	30	40	
80	90	100	110	120	130
AGARGSGEWDRLP--ACGGAAP--RSROPARPPYRVGGAG--QRLEFSRGRA---RGEAGARRAVSC					
--RKRSVELDQLPEQPLFLAASPASSTSPSPEDAADAGSGTGFQVAVPPPHGAASRRGAHLETESVAAFD					
50	60	70	80	90	100
140	150	160	170	180	190
SG---PRSRVDGEKR-----NSQVADGXSRRGTNOGETEGNL---YASLEARM-VGKEKXARACGGKTN					
SGASSPAAAFPGEKRAPAAPFSPAAAPAG---REMNKETLKLHWRMDRPERMIREKLKATCMPAWKHE					
120	130	140	150	160	170
200	210	220	230	240	250
PSYERWIXNBSLSXVSRGPKCGFTSFQPTQFSWQLPIRSHSIRIS----RSKEKXSPFSASEWQN					
WLERR-----NRRGP-VVVKPIPVKGDSENMHLAAESPGVQASAAAPSKRRRSPSPGNSPSGR					
190	200	210	220	230	240
270	280	290	300	310	320
HTTPKSPFTRWLLTIXPKGNPKCKQSDAGQTIVLTADRAXLFPD-----WRRQPRQXIPGVYWASE					
TVKSESQVR-----RKRVSPVFQS---GR-TIPERRA-PSPDGFSYSPSETNRR-----VNKMVRA-R					
250	260	270	280	290	
330	340	350	360	370	380
LQLCTWNLXSAL-CDAPGVSTRTF-RPNVMXNFKBF-XGXFV-----PDIS---QXAXLKQDSSIS					
LYLLQIQIPNSFLIGGSDPDNKYRVFIQPCQSCAHGTFCHLLFVMLRVFQLPSPDMLWKTLK-----					
300	310	320	330	340	350
390	400	410	420	430	440
XHHPEVCFTHVK-----FSYIVIIYFIKPRKHQKXRGTDVSVLLVGHAXXKRSYXVRRLQEQAAP----					
--NPEVSLFKYHSRRSSRIKAPSRNTI---QKFVSRMGNSTLSSSTSSSENSIKDEBQMCPICL					
370	380	390	400	410	420
450	460	470	480	490	500
-----PLHV-NLGRYKXKXRTFNMSPLXIXVEISXFLQPRVYKSGCFFFPQSCATAANRTAAAPGWITK					
LGMLDESLTVCEDGCR--NKLHHHCMS--IWAE-----ECRRNREPLICPLCRSKWRSHDFYSH					
430	440	450	460	470	480
520	530	540	550	560	570
E-SREQXPYSLMNSANPCLQRFESXAMDGVMWNGTRWLLTFXKLECEDRGDGPQASFPXQMGPAVKGWGEHW					
ELSSPVDSPSL-RAAQOQTVOQOLA-----GSR-RNOESNENLHYGTQ-----QTPPAYKDLAEFP					
490	500	510	520	530	540
590	600	610	620	630	640
KFWGQMKQPEWGSHQVFPDQYLRRCGGMLQRSVNGLCKPCLQSVRCFFKNIES--HAGIYSLPQSGKN					

> O <  
O|O Intelligence  
> O <  
FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4  
Results file 6168950\_x\_697898.res made by spaula on Thu 20 Feb 103 16:42:08-EST.

Query sequence being compared:US-09-359-756-1 (1-4693)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-359-756-1 (1-4693) with:  
File : US09697898mod.pgp



PARAMETERS			
Similarity matrix	Unitary	K-tuple	2
Translation frame	6		
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	500
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS			
Scores:	Mean	Median	Standard Deviation
	17	0	0.00
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00
Number of residues:			1495
Number of sequences searched:			1
Number of scores above cutoff:			1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.  
A 100% identical sequence to the query sequence was not found.

2000

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
1. US-09-697-898-3	Sequence 3. Application US	1495	97.66	0.00	5

1. US-09-359-756-1 (1-4693)  
US-09-697-898-3 Sequence 3, Application US/09697898

Initial Score	=	9	Optimized Score	=	66	Significance	=	0.00
Residue Identity	=	18%	Matches	=	93	Mismatches	=	293
Gaps	=		Conservative Substitutions	=	113		=	0
Translation Frames	=	5						

1060		1070	1080	1090	1100	1110	1120	1130
LLYGLLCSSEGRGIHRTQQLVAEIMRSPLRSTKGYXRFSSISLFCFNHAVVVLPAAVFTHCKTF								
						x	x	
						PSPEAGGGGALKAKA-----		
							10	

1140 1150 1160 1170 1180 1190 1200  
 FKHQAQNRTHLFILYAVXTXRCR-STRXXQMRXHXANKLLGVTKWNSDPDXATETVIFLEGTMLL-  
 ---SSARAAAGLL---REAGSGGERADWRRQ-----LRKRVSELD-----OLPEQPLFLA  
 20 30 40 50 60

1210 1220 1230 1240 1250 1260  
 ---KILASFEXHWXFXLKHPEHHXQNTCSCTAAVLPRNKHPIVYAVSSNQEXRVPVLOXV---  
 ASPPASSTSP-----SPE-----PADAAGSGTGPQV-AVPPHGAASRGGAHLTESVAAP  
 70 80 90 100 110 120

1270 1280 1290 1300 1310 1320 1330  
 QSGPHFVNTAVCFRLAIWXEAIXRGSSG--WCDSATLK-RHNGNSPSYSWRFPHCAT---XWGV-----  
 DSGASSPAAAPGGEKRAPAAPSPAAAPAGACRMENKETTILKGLHDDIDPEERETREKILKATCMAPWAGHEMLE  
 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200

RRRTAGFSWSRSTCLDLS-  
||  
||  
RRNRKPFVVVKPTPVKVGDSGEMNHLLAAESPGVEQASASPASKGRSPSPGNSPSGRTRKSESQGVRRKRVSS

1400 1410 1420 1430 1440 1450 1460  
FLPDHSLWTHILVQFFSFTHLTGGGCRRLGGSPLLPGLGRCCTGGAVERRRRLGK--VGAAP  
PVVFQSGRIT--PRRRASPDPGFSPSEETNR--RVNKMRLVLLQOIGPNSFLIGDSDPNKYRVFVIGP

1470 1480 1490 1500 1510 1520 1530  
AGGS--VGRHRRHLEAGETPCVCGLRGRGGRGGKKEERLLRQLVLTHTFHAQLQPPPPVRLAAPA  
QNCSCAGHTFCIHL---FWMLRVFLEPDPMLKRTLKNEF--VESLFQYHSSRRSRKAFPSR-----N

1540 1550 1560 X  
ARLPQSGRGRAARALEGSS-----AAACLR  
| | | | |  
TIQKFSRMS--N\$H\$TSS\$STSS\$S\$NSIKDEEFQMCPICULGNLDESLTVCEGCRNKLHHHC\$SIWA  
390 400 410 420 430 440 450

EECRNREPLICPLCRSKWRSHD  
460 470 480

Results of the initial comparison of US-09-359-756-1 (1-4693) with:  
File : US09697898mod.pep

100-  
-  
-  
50-  
-  
N U N E  
-  
-

## PARAMETERS

	Unitary	K-tuple
Similarity matrix	1	2
Translation frame	6	
Mismatch penalty	1	Joining penalty
Gap penalty	1.00	Window size
Gap size penalty	0.05	
Cutoff score	0	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	15	0	0.00

Times:	CPU	Total Elapsed
	00.00:00.00	00:00:00.00

```

Number of residues: 1495
Number of sequences searched: 1
Number of scores above cutoff: 1

```

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

